SEQUENCE LISTING

<110> ST GEORGE'S HOSPITAL MEDICAL SCHOOL

<120> DIAGNOSTICS AND VACCINES FOR MYCOBACTERIAL INFECTIONS
     OF ANIMALS AND HUMANS

<130> N74368A DMG IJB DP

<140> PCT/ GB 99/ 00849
<141> 1999-03-18

<150> UK 9806093.2
<151> 1998-03-20

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<170> PatentIn Ver. 2.1

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Pro Gly Leu Met Val Leu Cys Ala Glu Leu Ala Tyr Ser Arg Trp Arg
                165             170             175

Phe Glu Arg Phe Ala Ala Asp Glu Lys Ala Ser Thr Thr Gln Ala Met
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SEQUENCE LISTINGS

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501	GAAACTACTGATGTCCGGCGCTCCGATCGAGTATGTGCTAAAAGACAGTG
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SUBSTITUTE SHEET (RULE 26)

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1301   ATCCTCCCGCGCCGAGCCCAAGACCGGCTTTGTAA

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Sequence ID No.2

Total Residues = 444

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15   251   LPAWGGIHAIASNAARFAVMFSAGALLYQFRNVIPARWSFVAVGLIIVVV

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Sequence ID No. 3 = IS1612 positive strand.

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1601   GTCGACCTGCTCACCGGCTAACGCAGCTTCGGTCAGCAGCGGCACCGCAA

1651   GGTCGTCCTGAGCGTAGCCACAGAGGTTCTCCACGATGCCCTTCGATTGC

1701   GGATCCGCACCGTGGCAGAAGTCCGGAACGAAGCCATAGTGGGACGCGAA

1751   TCGCACATAATCCGGTGTTGGAACAACAACATTGGCGACGACACCACCTT

1801   TGAGGCAGCCCATCCGGTCGGCCAGGATCTTGGCCGGAACCCCACCGATC

1851   GCCTCGAGGGCTTCGGCTATCATCGCCTGCGTGGTCGAGGCTTTCTCGTC
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	1901	GGCGGCGAACCGCTCAAACCGCCACCGCGAATAGGCCAGCTCCGCGCATA
	1951	ACACCATCAGCCCCGGTGCCGCTTCGGCCCAATCCATCACCAGATAGTCA
	2001	CCGGGTGACCAGACCGCCGGACGGCGTTGATGCCGGTTAGCGTTGCGCCA
	2051	CCATACTTCCTGCTCGGCTACCAGGCGGCGGAAGTTACGGGCCGAGCCCT
5	2101	GATACCCGGCAGCTCGGGCGATCGGCAGCATCCGCTTCGCCGACATCTTG
	2151	CCGTGTGATTTCTCGACTCGGGTGGCGACTAGATCGGTGAACGCGTCGAG
	2201	GTTGCGTGGCCGTGGTTCCCGCGGGGGGCGCGCCACCGGCCTCGGCCCGCT
	2251	CGATGACCCGCTTGACCGTCTTGTGCGTACTACCGCACAGCTCGGCCGCG
	2301	CCGCGATACGACCCGACCTGGTGATACGCCGAAATGATGTTCATACGCTC
10	2351	CCTTGCAGACTTCAATAGAGCTCCCTGGGCGGTGATCAAGTGACAGTTGG
	2401	CGCTATCACCGTCACCGCCCAGGCCCTCAGCTCCCGGAAAAGACACGACG
	2451	AGCCCGCTAAGGAGTGGGGACTTCTACCTGGCCACCAGTGGGGACTTCCT
	2501	ACTGGCCACAGATGGGGACTTTCTCATGGCCATGGACATGCAC

(Total = 2543bp)

Sequence ID No.4 = IS*1612* negative strand to SEQ ID No.3.

	1	GTGCATGTCCATGGCCATGAGAAAGTCCCCATCTGTGGCCAGTAGGAAGT
20	51	CCCCACTGGTGGCCAGGTAGAAGTCCCCACTCCTTAGCGGGCTCGTCGTG
	101	TCTTTTCCGGGAGCTGAGGGCCTGGGCGGTGACGGTGATAGCGCCAACTG
	151	TCACTTGATCACCGCCCAGGGAGCTCTATTGAAGTCTGCAAGGGAGCGTA
	201	TGAACATCATTTCGGCGTATCACCAGGTCGGGTCGTATCGCGGCGCGGCC
	251	GAGCTGTGCGGTAGTACGCACAAGACGGTCAAGCGGGTCATCGAGCGGGC
25	301	CGAGGCCGGTGGCGCGCCCCCGCGGGAACCACGGCCACGCAACCTCGACG
	351	CGTTCACCGATCTAGTCGCCACCCGAGTCGAGAAATCACACGGCAAGATG
	401	TCGGCGAAGCGGATGCTGCCGATCGCCCGAGCTGCCGGGTATCAGGGCTC
	451	GGCCCGTAACTTCCGCCGCCTGGTAGCCGAGCAGGAAGTATGGTGGCGCA
	501	ACGCTAACCGGCATCAACGCCGTCCGGCGGTCTGGTCACCCGGTGACTAT
30	551	CTGGTGATGGATTGGGCCGAAGCGGCACCGGGGCTGATGGTGTTATGCGC

<pre>
  601   GGAGCTGGCCTATTCGCGGTGGCGGTTTGAGCGGTTCGCCGCCGACGAGA

  651   AAGCCTCGACCACGCAGGCGATGATAGCCGAAGCCCTCGAGGCGATCGGT

  701   GGGGTTCCGGCCAAGATCCTGGCCGACCGGATGGGCTGCCTCAAAGGTGG

  751   TGTCGTCGCCAATGTTGTTGTTCCAACACCGGATTATGTGCGATTCGCGT

5 801   CCCACTATGGCTTCGTTCCGGACTTCTGCCACGGTGCGGATCCGCAATCG

  851   AAGGGCATCGTGGAGAACCTCTGTGGCTACGCTCAGGACGACCTTGCGGT

  901   GCCGCTGCTGACCGAAGCTGCGTTAGCCGGTGAGCAGGTCGACCTACGTG

  951   CCCTCAACGCCCAGGCGCAACTATGGTGCGCCGAGGTCAATGCCACGGTC

 1001   CACTCGGAGATCTGCGCCGTGCCCAACGATCGCTTGGTTGACGAGCGCAC

10 1051 CGTCTTGAGGGAGCTGCCCTCGCTGCGGCCGACGATCGGCTCGGGGTCGG

 1101   TGCGCCGTAAGGTCGACGGCCTCTCGTGCATCCGTTACGGCTCAGCTCGT

 1151   TACTCGGTGCCTCAGCGGCTCGTCGGTGCCACCGTGGCGGTGGTGGTCGA

 1201   TCATGGCGCCCTGATCCTGTTGGAACCTGCGACCGGTGTGATCGTGGCCG

 1251   AGCACGAGCTCGTCAGCCCAGGTGAGGTGTCCATCCTCGATGAACACTAC

15 1301 GACGGACCCAGACCCGCACCCTCGCGTGGTCCTCGCCCGAAAACCCAAGC

 1351   AGAGAAACGATTCTGCGCATTGGGAACCGAAGCGCAGCAGTTCCTCGTCG

 1401   GTGCTGCTGCGATCGGCAACACCCGACTGAAATCCGAACTCGACATTCTG

 1451   CTCGGCCTTGGCGCCGCCCACGGCGAACAGGCTTTGATTGACGCGCTGCG

 1501   CCGGGCGGTTGCGTTTCGCCGGTTCCGCGCTGCCGACGTGCGCTCGATCC

20 1551 TGGCCGCCGGCGCCGGCACCCCACAACCCCGCCCCGCCGGCGACGCACTC

 1601   GTGCTCGATCTGCCCACCGTCGAGACCCGCTCGTTGGAGGCCTACAAGAT

 1651   CAACACCACCGACGGGACGGCCTCATGACCACCGCTGCCAAGCCGGTGGC

 1701   ACCGTCCTCGGCGGCACCGCTGGCTGCTGACCTTGACGCGGCGCTGCGGC

 1751   GGTTGAAGCTGGCCACGGTGCGCCGCAACGCCGCCGAGGTGTTGCAAGTC

25 1801 GCCAAGACGCAACGCTGGACACCGGAGGAGATCCTGCGGACGTTGGTTGA

 1851   GGCCGAGATCGCTGCCCGCGATGCCTCCAACACCGCCAACCGTCTCAAGG

 1901   CCGCAGCCTTCCCGGTCACCAAGACCCTCGACGGGTTCGACGTCACCGGA

 1951   TCGTCGATCACCGCAGCCACGTTCGACTACCTGTCGAGCCTGGAATGGAT

 2001   TCGGGCACAACAGAACCTGGCGGTCATTGGCCCACCTGGTACGGGCAAAA

30 2051 GTCACCTGCTCATCGGCTGCGGGCACGCTGCCGTCCACGCCGGATTCAAA
</pre>

2101	GTCCGCTACTTCACCGCCGCCGACCTGATCGAGGTCCTCTACCGCGGCCT
2151	GGCCGACAACACCGTCGGCAAGATCATCGACACCCTGCTCCGCGCGGATC
2201	TGGTCATCTTGGACGAGATCGGCTTCGCCCCGCTCGACGACACCGGGACT
2251	CAACTGTTGTTCCGGCTCGTGGCTGCCGGCTACGAGCGCCGCTCCCTGGC
2301	CATCGCCTCGCATTGGCCCTTCGAACAATGGGGGCGATTCCTGCCCGAGC
2351	ACACCACCGCCGCCAGCATCCTCGATCGGCTGCTGCACCACGCCAGCATC
2401	GTCGTCACCTCCGGCGAGTCCTACCGGATGCGCCACGCCGACCACAAGAA
2451	GGGAGCCGCCAAGAATTAGCCAACCACCCGCAGCGGAGTGGGGACTTCTG
2501	CTGGCCACCAGCGGGGACTTCTACTTGGCCATTGACAGTGCAT

(Total = 2543bp)

Sequence ID No.5 = Amino acid sequence of polypeptide designated istA

encoded by Seq ID No.4.

1	VSFPGAEGLGGDGDSANCHLITAQGALLKSARERMNIISAYHQVGSYRGA
51	AELCGSTHKTVKRVIERAEAGGAPPREPRPRNLDAFTDLVATRVEKSHGK
101	MSAKRMLPIARAAGYQGSARNFRRLVAEQEVWWRNANRHQRRPAVWSPGD
151	YLVMDWAEAAPGLMVLCAELAYSRWRFERFAADEKASTTQAMIAEALEAI
201	GGVPAKILADRMGCLKGGVVANVVVPTPDYVRFASHYGFVPDFCHGADPQ
251	SKGIVENLCGYAQDDLAVPLLTEAALAGEQVDLRALNAQAQLWCAEVNAT
301	VHSEICAVPNDRLVDERTVLRELPSLRPTIGSGSVRRKVDGLSCIRYGSA
351	RYSVPQRLVGATVAVVVDHGALILLEPATGVIVAEHELVSPGEVSILDEH
401	YDGPRPAPSRGPRPKTQAEKRFCALGTEAQQFLVGAAAIGNTRLKSELDI
451	LLGLGAAHGEQALIDALRRAVAFRRFRAADVRSILAAGAGTPQPRPAGDA
501	LVLDLPTVETRSLEAYKINTTDGTAS

(Total = 526 aa)

Coded by nucleotides 98 - 1678 of seq ID No 4.